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10426.099 Million cell updates/sec
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CD295681 StrPu691.
CD296311 StrPu691.
CF919042 Bflor531.
BI387857 BFL26 002
BZ894814 H94 0102
CB656525 OSJNEC10P
CB683938 OSJNEC12P
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CF488266 POL1_48_F	CF487230 POL1_42_C	CF432900 NIT1_19_E	CCC1_34	4	CCCI 24	0	CCC1_51	CCC1_13	CF481017 POL1_69_B	6	0V1_38	CG440030 OGVHP10TH	CN127041 RHOH1_20_		BE040798 OF11G11 O	CD429468 ETH1_4_D0	CA269770 SCMCRT308	CB902534 tric030xk	CB903555 tric035xc	CA227320 SCJLFL301

ALIGNMENTS

REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION JÖURNAL MEDLINE PUBMED Email: panopoulemolgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONFP) to reduce sequencing redundancy. According to the ONFP
procedure, clones giving the same hybridisation pattern with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well the coordinates of the
rest of the clones assigned to the same fingerprint cluster as the
clone from which the above EST is generated is available at the
amphicous project site at: http://www.molgen.mpg.de/amphicous/
Clones and filters are distributed via the Resource Center/Primary
Database of the German Genome Project (http://www.rzpd.de) Insert Length: 1200 Std Error: 0.00 Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86 FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3'
BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3 laboratory 145, dept.Lehrach Max-Planck-Institut fuer Molekulare Genetik Ihnestr.63-73, D-14195 Berlin, Germany Panopoulou, G., Hennig, S., Groth, D., Krause, A., Poustka, A.J Herwig, R., Vingron, M. and Lehrach, H. New evidence for genome-wide duplications at the origin of Branchiostoma floridae (Florida lancelet) Branchiostoma floridae mRNA sequence. BI376242 BI376242.1 GI:30911206 BI376242 623 bp mRNA linear EST 26-AUG-200: BFLG3 000038 Amphioxus 5-6 hrs cDNA library (Name convention: BFLG or MPMGp498) Branchiostoma floridae cDNA clone MPMGp498A1518 5', Tel: +49 30 8413 1235 Fax: +49 30 8413 1128 PCR PRimers vertebrates using an amphioxus Contact: Panopoulou G **Genome Res. 13 (6A), 1056-1066 (2003)** Eukaryota; Metazoa; 2683279 (bases 1 to 623) Chordata; Cephalochordata; Branchiostomidae; gene set and completed animal 3' (M13FSP) Poustka, A.J., EST 26-AUG-2003 one

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RESULT 2
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Matches 430; Conserv
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/mol_type="mRNA"
/db xref="taxon:7739"
/clone="MMPKg9498A1518"
/tissue_type="whole embryo"
/dev_stage="5-6 hrs (gastrula stage)"
/lab_host="E.coli, XL1 blue"
/clone_lib="Amphioxus 5-6 hrs cDNA library (Name convention: BFLG or MPKg9498)"
/note="Vector: pSport1; Site 1: SalI, KpnI, EcoRI (5');
Site 2: NotI, BamHI, HindIII (3'); OligodT primed and directionally cloned in pSport1 vector using a NotI (5'-pGACTAGTTCTAGATCGCGAGCGGCCCC (T)15-3' and a SalI 5'-TCGACCCACGCGTCCG-3'adapters (Gibco BRL)."
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1 (bases 1 to 470)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,F., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?t1=IL&t2=IL-BT109-002.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq
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Fax: +55-11-2707001
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Homo sapiens (human)
Homo sapiens
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ACCGCGAGTGGGACCTGCTGAAGTACCGCTCCTTCGGCTATGGCCACTCCTTCGGCGTGC
                                                                                                                                                                               ATGTCGATGACGCCAGCCTCGACATCTGGGAGAAGAACGTGGCCGTGCATCGCCGCGGGC
                                                                                                                                                                                                                                                CACCTTCCCGATGATCTTCGGC-TACTACACCGCGCTGGAGCGCACGCTGTTCTGCGACC
                                                                                                                                                                                                                                                                                                           TGGGGCGCATAACCCGGGTGACCAGCCGCCGGGTGGGAAAAGCGAGATCCTCAGCCTCAA
                                                                                                                                                                                                                                                                                                                                CGGCGCGCACAATCCGGTCACCAACCGCATCGTGCAATCCGGGGACATCCTTTCGCTCAA
                                                                                                                                                                                                                                                                                                                                                                                          GATCCCCTGAATGGCGCTGATAACACCTTGGACNTGGTTCCAGTCCGGGTTCAACACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                   GTTCCCCTTCGTGGAGCTGATGGACACCTGGACCTGGTTCCAGTCGGGCATCAACACCGA
                                                               TGAAACTGGTGCGCCCCGGCATGCGCTGCAGCGATATCGCTCGGGAACTGAACGAGATCT
                                                                                        TCGAGCTGATCAAGCCGGGGCGCGCGCTGCAAGGACATCGCCATCGAGCTCAACGAGATGT
                                                                                                                                                                                                                           TTGCTTCCCGATGATCGCCGGCATATTACACCGCGTTGGAGCGCACGCTGTTCCTCGACC
                                                                                                                                               ACTGCCCGGACGAGTACCTACGCCTGTGGCAGGCCAACGTCGAAGTGCACGAAGCCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer: puc 18 forward.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="Adult"
/clone lib="BBT109"
/clone lib="BBT109"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and clnA amplification were performed under low
stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 221; DB 1; Lo
Pred. No. 3.2e-38;
0; Mismatches 137;
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01509-010,

Sao

Paulo-SP,

ORF

Length

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Indels

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Gaps

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808 336

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REFERENCE
AUTHORS
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CD307119/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: poustka@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above EST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/ag_seaurchin/.cDNa
clones and filters are distributed via the Resource Center/Primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Max-Planck-Institut fuer Molekulare Innestr.63-73, D-14195 Berlin, Germa Tel: +49 30 8413 1235
Email: poustka@molgen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pustka, A.J., Groth, D., Hennig, S., Thamm, S., Cameron, A., Ber Poustka, A.J., Groth, D., Hennig, S., Thamm, S., Cameron, A., Ber Reinhardt, R., Herwig, R., Panopoulou, G. and Lehrach, H. Generation, annotation, evolutionary analysis, and database integration of 20,000 unique sea urchin EST clusters Genome Res. 13 (12), 2736-2746 (2003)

Contact: Poustka AJ
Laboraty 145, dept. Lehrach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strongylocentrotus purpuratus cDNA MRMGp69180990, MPI_SURUDI_90E9 5', m CD307119.1 GI:34752168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP) 5'-seq BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13RSP) 3'-seq Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86
High quality sequence stop: 494.
Location/Qualifiers
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494 bp mRNA linear EST 16-SEP-2003
StrPu691.009486 Sea urchin larva CDNA library MPMGp691
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                                                                                                          /clone="MPMGp691E0990;MPI_SURUDI_90E9"
/tissue_type="whole larva"
/dev_stage="larva 2-3 weeks"
/lab host="B.coli, XLI blue"
/clone_lib="Sea urchin larva cDNA library MPMGp691"
/clone="Vector: pSport1; Site_1: Not1; Site_2: Sal1; Random primed and directionally cloned in pSport1 vector using a Not1 (5'-pGACTAGTTCTAGATCGCGAGCGGCCCC (T)15-3' and a Sal1 5'- TCGACCCACGCGTCCG-3'adapters (Gibco BRL)"
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
   17.1%;
   Score 207.8; DB 6; Pred. No. 2.6e-35;
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                            Length 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 312;
                                                                                                                                                                                                                                                                Contact: Poustka AJ laboraty 145, dept.Lehrach Max-Planck-Institut fuer Molekulare Genetik Ihnestr.63-73, D-14195 Berlin, Germany Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
Email: DONEFTRACT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56
Email: postka@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 Bmer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above EST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/ag_seaurchin/.cDNA
clones and filters are distributed via the Resource Center/Primary
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strongylocentrotus purpuratus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strongylocentrotidae; Strongylocentrotus
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RESULT 5
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LOCUS
DEFINITION
                                                                          REFERENCE
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ORGANISM
                                                                                                                                                                                                                                 ACCESSION
VERSION
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Best Local Sim
Matches 282;
         TITLE
                                                   AUTHORS
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                                                                                                                                                                                                                          CD296311
519 bp mRNA linear EST strbu691.007706 Sea urchin larva CDNA library MPMGp691 Strongylocentrotus purpuratus cDNA clone MPMGp691N1215;MPI_SURUDI_15N12 5', mRNA sequence.
CD296311
CD296311.1 GI:34747388
                                                                                   Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota, Metazoa, Echinodermata, Eleutherozoa,
Echinoidea, Euechinoidea, Echinacea, Echinoida,
Strongylocentrotidae, Strongylocentrotus.
1 (bases 1 to 519)
Poustka, A.J., Groth, D., Hennig, S., Thamm, S., Camero Reinhardt, R., Herwig, R., Panopoulou, G. and Lehrach, Generation, annotation, evolutionary analysis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP) 5'-seq BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13RSP) 3'-sec Seq primer: 5' GCTATTACGCCAACTGGCGAAAGGGGGATGTG 3' (M13FSP) High quality sequence stop: 442.
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PCR PRimers
FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP) 5'-seq
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/tissue_type="whole larva"
/dev_stage="larva 2-3 weeks"
/lab_host="E.coli, XL1 blue"
/clone_lib="Sea urchin larva cDNA library MPMGp691"
/note="Vector: pSportl; Site 1: Not1; Site 2: Sall; Random primed and directionally cloned in pSportl-Vector using a Not1 (5'-pGACTAGTTCTAGATCGCGAGCGGCCCC (T)15-3' and a Sall 5'- TCGACCCACGCGTCCG-3'adapters (Gibco BRL)"
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/db_xref="taxon:7668"
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/mol_type="mRNA"
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Pred. No. 4.4e-31;
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                           Cameron, A., ehrach, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           procedure, clones that display the same hybridisation matrix with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per ONF cluster is selected for sequencing. The size of each cluster is an indicator of the frequency of a transcript in the analysed library. The cluster size as well as the coordinates of the other clones assigned to the same ONF cluster as the clone from which the above EST is generated is available at the sea urchin project web site at: http://www.molgen.mpg.de/ag_seaurchin/.cDNA clones and filters are distributed via the Resource Center/Primary Database of the German Human Genome Project (http://www.rzpd.de) PCR PRIMEERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         integration of 20,000 unique sea urchin EST clusters genome Res. 13 (12), 2736-2746 (2003)
Contact: Poustka AJ
laboraty 145, dept.Lehrach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13FSP)
BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP)
Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86
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Fax: +49 30 8413 1128
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The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
CGCATCGGCATCGAGTTCGACCACGTCAATCTCGACTTCCGCCGCCGAGCTCGAGGAAGCC
                                                     GATTGGCATCGCGACAACTTCTGGAGCGCCGTTCGGCACCTGCTCGGCAACGCTTCGGNG
                                                                                    GACTGGCGCCGCGACAATTTCTATCGCGCCCGT---GCGCCAGCTGACCACGGGCGCCAAG
                                                                                                                                                          GTCGACAGCGGCCAGGCCTGGCGGAGATCACCCGTGAGCGACGATGTGGTCATCTACACG
                                                                                                                                                                                         ATCGACGGCGGCCAGCCCTGGCG------CCGCAGCTTCGGCGACAACATCACCTACACCT
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/tissue_type="whole larva"
/dev_stage="larva 2-3 weeks"
/lab host="p.coli, XL1 blue"
/clone_lib="Sea urchin larva cDNA library MPMGp691"
/note="Vector: pSportl; Site_1: Not1; Site_2: Sal1; Random primed and directionally cloned in pSportl vector using a Not1 (5'.pGACTAGTTCTAGATCGCGAGCGGCCCC (T)15-3' and a Sal1 5'- TCGACCCACGCGTCCG-3'adapters (Gibco BRL)"
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/db_xref="taxon:7668"
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Pred. No. 8.9e-17;
0; Mismatches 208;
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                                                                                                                                                                                                                                                                                                                                Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +49 30 8413 1235

Fax: +49 30 8413 1128

Email: panopoul@molgen.mpg.de

Email: panopoul@molgen.mpg.de

The library was characterised by oligonucleotide fingerprinting

(ONFP) to reduce sequencing redundancy. According to the ONFP

procedure clones giving the same hybridisation pattern with a

battery of 200 8mer oligonucleotides are grouped into clusters. One

clone per cluster is selected for sequencing. The size of each

cluster is an indicator of the frequency of a transcript in the

analysed library. The cluster size as well as the coordinates of

all clones assigned to the same fingerprint cluster as the clone

from which the above EST is generated is available at the amphioxus

project site at http://www.molgen.mpg.de/amphioxus.

Clones and filters are distributed via the Resource Center/Primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CP919042 551 bp mRNA linear I Bflor531.000127 Amphioxus 26 hrs cDNA library (Name o BFL26 or MPWGp531) Branchiostoma floridae cDNA clone MPMGp531L07115;BFL26 115L7 5', mRNA sequence.
CF919042
                                                                                                                                                                                                                                                                                                                                                                                           FORMARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (
BACKWARD: 5' GCTATTACGCCAGCTGGCGAAGGGGGATGTG 3' (
INSET Length: 1200 Std Error: 200.00
Seq primer: 5'-CCGGTCCGGAATTCCCGGGT-3' pSport3/86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laboratory 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Thnestr.63-73, D-14195 Berlin, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 13 (6A), 1056-1066 (2003)
22683279
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New evidence for genome-wide duplications at the origin of vertebrates using an amphioxus gene set and completed anima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Branchiostoma floridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database of the German Genome Project (http://www.rzpd.de).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Panopoulou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CF919042.1 GI:38190244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Branchiostoma floridae (Florida lancelet)
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                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 551.
/Btrail="wild type"
/db xref="texon:7739"
/clone="MPMGp531L07115;BFL26_115L7"
/tissue_type="whole embryo"
/dev_stage="26 hrs (neurula stage)"
/lab_host="Escherichia coli, xtl) blue"
/lab_host="Bscherichia coli, xtl) blue"
/clone_lib="Amphioxus 26 hrs cDNA library (Name
/clone_lib="Amphioxus 26 hrs cDNA library (Name
/convention: BFL26 or MPMGp531)"
/note="Vector: pSpport1; Site 1: Sal1, Kpn1, EcoRI (5');
/note="Vector: BamHI, HindIII"
Site_1: NotI, BamHI, HindIII"
Site_2: NotI, BamHI, HindIII'
(5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC (T)15-3' and a SalI 5'-
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                 mol_type="mRNA"
                                                                                                                                                                                                                                                                                                      organism="Branchiostoma"
                                                                                                                                                                                                                                                                                                           floridae"
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BI387857
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AUTHORS
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Panopoulou G
laboratory 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
                                                                                                                                                                                                                                                                                                                                                                                           Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 13
22683279
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266 CCTGGCGCCGCAGCTT 281
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                                                                                                                                                                                                                                                                                                                                                GCCAAAACGACGTTCGCGGCTGGATGGCCAAGAACAATGTCGATGCGGCGCTGTTCACCT 145
                                                                                                    GGCTGGTCGTCACCATGGACAAAGTGCTCTTCTTATCCCCCAGCCGTTGACGGTGGTCAGC
                                                                                                                                                    CTTATCACTGCATCAACTACTATTCCGGCTGGCTGTACTGCTATTTCGGACGCAAGTACG
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CCTGGAGAAGGAGCAT 541
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Pred. No. 6.9e-08;
D; Mismatches 108;
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525 265 465 205

Panopoulou,G., Hennig,S., Groth,D., Krause,A., Poustka,A.J., Herwig,R., Vingron,M. and Lehrach,H.

New evidence for genome-wide duplications at the origin of vertbbrates using an amphioxus gene set and completed animal BFL26 002560 Amphioxus 26hr cDNA library (Name convention: BFL26 or MPMGp531) Branchiostoma floridae cDNA clone MPMGp531L07115 5', mRNA Branchiostoma floridae BI387857.1 GI:30922696 Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae; Branchiostoma floridae (Florida lancelet) (bases 1 to 553) 553 bp mRNA linear EST 26-AUG-2003

Email: panopoul@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONFP) to reduce sequencing redundancy. According to the ONFP
procedure, clones giving the same hybridisation pattern with a
battery of 200 Bmer oligonucleotides are grouped into clusters. One
clone per cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well the coordinates of the
rest of the clones assigned to the same fingerprint cluster as the
clone from which the above EST is generated is available at the
amphioxus project site at: http://www.molgen.mpg.de/amphioxus/
clones and filters are distributed via the Resource Center/Primary Database of the German Genome Project (http://www.rzpd.de) FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (MI3RSP)

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TITLE
JOURNAL
COMMENT
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AUTHORS
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VERSION
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BZ894814
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Best Local S
Matches 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 TGAAATGGCACAACGGCGAGAAAGATTATTCGCCGTTTTTCGGATGCCGAGATGACCCGCC
                                                                                                                       Low-pass Sequencing for Microbial Unpublished (2003)
Contact: Go Y
                                    Email: ygoo@systemsbiology.org
Seq primer: M13 Forward
Class: shotgun.
                                                                                                                                                                                                                                                                                     BZ894814
Hg4_0102 Hg pUC18 Library genomic survey sequence.
BZ894814
                                                                                                                                                                Goo, Y., Roach, J., Glusman, G., DasSarma, S., Ng, W.V. and Hood,
                                                                                                                                                                                                                   Halobaculum gomorrense
Archaea; Euryarchaeota; Halobacteria;
                                                                                                                                                                                                                                              Halobaculum gomorrense
                                                                                                                                                                                                                                                                         BZ894814.1
                                                                           Institute for Systems Biology
1441 North 34th Street, Seattle,
Tel: 206 732 1412
Fax: 206 732 1299
                                                                                                                                                                                                         Halobacteriaceae; Halobaculum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.9%;
Similarity 57.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    CCTGGCGCCGCAGCTT
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                                                                                                                                                                                            (bases 1 to 524)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="MPMGp531L07115"
/tissue_type="whole embryo"
/dev_stage="26 hrs (neurla stage)"
/lab host="E.coli, XL1 blue"
/clone_lib="Amphioxus 26hr cDNA library (Name convention:
BFL26 or MPMGp531)"
/note="Vector: pSport1 (Gibco BRL); Site_1: Sall, KpnI,
EcoRI (5'); Site_2: NotI, BamHI, HindIII (3'); OligodT
primed and directionally cloned in pSport1 vector using a
NotI (5'-pGACTAGTTCTAGATCGCGACCGCCCC (7)15-3' and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sall 5'- TCGACCCACGCGTCCG-3'adapters (Gibco BRL)."
/organism="Halobaculum
                         Location/Qualifiers
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                                                                                                                                                                                                                                                                         GI:33345290
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                                                                                                                                                                                                                                                                                                                                                                                                                    281
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Pred. No. 6.9e-08;
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                                                                                                                                                                                                                                                                                                              524 bp DN
/ Halobaculum
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 gomorrense"
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                                                                                                                                                      Comparative
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                                                                                                                                                                                                                                                                                                                            DNA
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                                                                                                                                                                                                                                                                                                                            linear
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AUTHORS
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EST.
                                                                                          PCR PRimers
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Contact: Rod Wing
Arizona Genomics Instit
University of Arizona
Biological Sciences We
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Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
                                                                                        BACKWARD: gga aac agc tat gac cat g
plate: 10 row: P column: 11
Seq primer: gta aaa cga cgg cca gtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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OSJNEC10P11.f OSJNEC Oryza sativa (japonica
clone OSJNEC10P11 5', mRNA sequence.
CB656525
                                                                                                                                                                                                                                                   Tel: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                           FORWARD: gta aaa cga cgg cca gtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehrhartoideae;
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                                                                                                                                                                                                                        http://genome.arizona.edu
1. .722
/organism="Oryza sativa (japonica cultivar-group)"
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/strain="ATCC 700876"
/db xref="texon:43928"
/clone lib="Hg pUC18 Library"
/note="Vector: pUC18; Site_1: Smal; A shotgun library was constructed from Halobaculum gomorrense genomic DNA using pUC18/Smal/BAP plasmid"
                                                                  Location/Qualifiers
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Pred. No. 6.8e-05;
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RESULT 10
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DEFINITION
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AUTHORS
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ORGANISM
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Matches 260;
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OSJNEf12P21.f OSJNEf Oryza sativa (japonica cultivar-group)
Clone OSJNEf12P21 5', mRNA sequence.
CB683938
                                        Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                Jantasuriyarat,C.
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                                                                                                                                                                                                                                                        AAGGTGCTCACCAGCTTCAAGACCGGCGACGTCGCCGG
                                                                                                                                                                                                                                                                                ATGGAGCCGATGGTGATGCTGCCGGAGGGCATGCCCGG 1109
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                           (bases 1 to 722)
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/note="Vector: pBluescript II I
XhoI; 6 hrs after innoculation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEC10P11"
arat, C., Lu, G., Gowda, M., Hatfield, J., Zh
Dean, R., Soderlund, C., Wing, R. and Wang,
                                                                                                                             GI:29687663
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45.0%;
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Pred. No. 8.5e-05;
0; Mismatches 318
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Rice_Blast (C9240-1)"
              Zhou, B.,
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Best Local S
Matches 259
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Contact: Rod Wing
Arizona Genomics Instit
University of Arizona
Biological Sciences Wes
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Plate: 12 row: P COlumn: 21
Seq primer: gta aaa cga cgg cc
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 520 626 3967
Fax: 520 621 9288
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ACCGACGTGCCGACGTACGTGATGTTCTACGACGAGCAAGCGGCGAACTACCCGGGCGGC
                               gccggcgrgaagcrgcggaggacarcgacaccgagcrgaagcccggcarggrgercrcc
                                                                         CGGCGCTACGCCGGCGTGATCGACCTCGTCAACTTCCAGTTCTACGGCTACGGCGACAAC
                                                                                                           TACCGCTCCTTCGGCTATGGCCACTCCTTCGGCGTGCTGTGCCACTACTACGGTCGCGAG
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nilarity 44.8%;
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/dev stage="3 week"
/lab_host="DH10B"
/clone_lib="QSJNEf"
/note="Vector: pBluescript I
XhoI; Uninfected Control"
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                    795
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                         GATGCGCACCATCAAGTCGCTCGAAGAGCAGAAGCTGATCCGCGAAGGCGCCCGCGTGTG
                                                                                                                                                          GCTCGAGGAAGCCCTA---CCGGGCGTCGACTTCGTCGACATCAGCCAGCCCTCGATGTG
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/clone_lib="RPCI-98"
/note="end : TET3"
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 33 1 69 47 54 00 Fax: 33 1 69 47 54 10
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                       TCCGGCTCCCTGCCCCTCAGCGCGCTCCTGCTCGCCGCGCGCCACATGCCCGACGCGGCC
                                                                               ATCGAGCTCAACGAGATGTACCGCGAGTGGGACCTGCTGAAGTACCGCTCCTTCGGCTAT 969
                                                                                                                                                    CAGTCGGGCATCAACACCGACGGCGCGCACAATCCGGTCACCAACCGCATCGTGCAATCC
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/cultivar="recital"
/db_xref="taxon:4565"
/clone="AZO2111114"
/tissue_type="root"
/clone_lib="AZO2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Bo
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: gta aaa cga cgg cca gtg
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: gta aaa cga cgg cca g
BACKWARD: gga aac agc tat gac
Plate: 15 row: O column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between rice and Magnaporthe grisea Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazu Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G. Large-scale identification of ESTs involved in the interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CB659172 812 bp mRNA CSJNEC15018.f OSJNEC Oryza sativa (japonica clone OSJNEc15018 5', mRNA sequence.
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Jantasuriyarat, C., Lu, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
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TTCCCCTTCGTGGAGCTGATGGACCTGGACCTGGTTCCAGTCGGGCATCAACACCGAC
                                                      CCCGAGCATGAAGTGGCGATCGCCACCACCAATGCGATGATCCGCGAGATCGCCAAAATCG
                                                                                                                       GGAGACGGCGGCGCGCGCGCGCGTCGGGAGCTGGGCGACGTTCTTGCAGCACGGCCTG
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                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                           /clone_lib="OSJNEc"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site,
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site,
XhoI; 6 hrs after innoculation with Rice_Blast (C9240-1)
                                                                                                                                                                                                                                                                                                                                 /tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                              1. .812
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/clone="OSJNEc15018"
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a; Poales; Poaceae;
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305-8602, Japan
Tel: 81-298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Institute of Agrobiological Resources Rice Genome Research Program, Kannondai 2-1-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 604)
Sasaki, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: tsasaki@abr.affrc.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Takuji Sasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                           GCGCACAATCCGGTCACCAACCGCATCGTGCAATCCGGCGACATCCTTTCGCTCAACACC 753
                                                      CTCTACTGGATGGGCGGCCTCGACCCGCGCGCCCTTCCTCCTCCTCCTCGTC
                                                                                      GCGCGCACCGCCGGCCGACCTACCCATGGAGCTCGCCCTCCCCACCGCCTTCGTCGTCATC
                                                                                                                                                                                                                            CCCTTCGTGGAGCTGATGGACACCTGGACCTGGTTCCAGTCGGGCATCAACACCGGACGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa
/mol_type="mRNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                               /tissue_type="mature leaf"
/clone_lib="Rice mature leaf"
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/clone="821656"
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Pred. No. 0.0065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mmprattaga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science, plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences or nresented as their reverse complement and have been trimmed to
                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: Sug5 (CTTCTGCTCTAAAAGCTGCG).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Rathore, K., Eastman, A. and Pratt, L.H.

An EST database from Sorghum: callus culture and cell suspension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 668)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD255047 668 bp mRNA linear EST 21-MAY-2003 CCC1 37_H01.g1 A007 Callus culture/cell suspension Sorghum bicolor cDNA clone CCCI_37_H01_A007 5', mRNA sequence.
CD225047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other_ESTs: CCC1_37_H01.b1_A007
Contact: Cordonnier-Pratt MM
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706 583 0210
                           /db_xref="taxon:4558"
/clone="CCC1 37 H01 A007"
/lab_host="DH108-T1 phage-resistant E. coli"
/clone lib="CR11us culture/Cell suspension"
/clone lib="Callus culture/Cell suspension"
/note="Vector: pME18S-FL3; Site 1: XhoI; kite 2: XhoI;
library was prepared from a mixture of polyA+ RNA from callus culture tissue and cells in suspension culture.
Double-stranded cDNA was cloned unidirectionally into
different DraIII sites of the pME18S-FL3 vector (5-prime
                                                                                                                                                                                                                                                                                                    cultivar="RTx430"
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                                                    CAACCACAACGCCGACTCCGGCCGGGACTTCACCTGAGTGCAGGCGCTCGGCGTCACCTT
                                                                              CACCATCAAGTCGCTCGAAGAGCAGAAGCTGATCCGCGAAGGCGCCCGCGTGTGTGACGT
                                                                                                         GGACGAGAGCTTCTGCCTCGTCTCCGACGACCGCCTCCACATCAACGCGCGGTTCATGGG
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nilarity 47.5%;
Conservative
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Pred. No. 0
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Search completed: November 19, Job time: 4241 secs 2004, 19:22:01

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SUMMARIES		
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26.2	•	46.5	52.3	52.4	52.8	80.3	80.5		90:6	80.6	80.7	81.0	81.0	97.8	99.9	99.9	99.9	99.9	99.9	99.9	Query Match
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5.1	5.1	5.2	5.2	5.2	5.2	5.2	5.3	5. U	5.4	5.4	5.4		წ	5.6			5.7	5.7	6.0	6.0	6.1	6.1	6.1
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ALIGNMENTS

RESULT 1 AAT61367 Creatinine amidinohydrolase coding sequence 17-APR-1997 AAT61367; AAT61367 standard; DNA; 1212 BP. (first entry)

Thermal stability; creatinine amidinohydrolase; creatine; sarcosine; urea; blood; ds.

JP08308579-A. Alcaligenes faecalis.

16-MAY-1995; 26-NOV-1996. 95JP-00117283

(TOYM) TOYOBO KK.

16-MAY-1995;

95JP-00117283

P-PSDB; AAW11861. WPI; 1997-059698/06.

Gene coding for creatinine amidinohydrolase - used to quantify blood or urinary creatinine as a disease indicator.

Claim 4; Page 10-11; 12pp; Japanese.

which has a low Km value for creatine. The creatinine amidinohydrolase has the following physicochemical properties: (a) action: converts creatine and water into sarcosine and urea; (b) optimum tempo: 40-45 deg.C; (c) optimum pH: 8.0-9.0; (d) thermal stability: about 50 or less (pH 7.5, 30 mins); (e) stable pH: a Ph range of about 4-10; (f) Km value: about 15.2 mM; (g) mol. wt: about 4300 (SDS-PAGE); and (h) isoelectric point: about 3.5. The creatinine amidinohydrolase may be used in the quantification of blood or urinary creatinine and creatine as an This sequence encodes a thermally stable creatinine amidinohydrolase indicator of various diseases

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TTCGGCTATGGCCACTCCTTCGGCGTGCTGTGCCACTACGGTCGCGAGGCCGGCGTG
                                                                                                     ACCGACTGGCGCGACAATTTCTATCGCGCCGTGCGCCAGCTGACCACGGGCGCCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.9%;
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Pred. No. 1.5e.
0; Mismatches
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No. 1.5e-195;
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A novel creatine amidinohydrolase enzyme has been developed which catalyses the reaction of creatine with water to form sarcosine and urea, is stable at temperatures of up to 50 degrees Celsius (pH 7.5, 30 minutes) and has an optimum temperature of 40-50 degrees (pH 7.5, 30 pt mum pH of 8-9, a Km value for creatine of 3.5-10 mM in a binding assay using sarcosine oxidase and peroxidase, a molecular weight of 43 kD by SDS-PAGE and an isoelectric point of 3.5. The present sequence encodes creatine amidinohydrolase derived from Alcaligenes faecalis strain TE3581 (FERM p-14237) which is the wild type creatine amidinohydrolase to be mutated in the present invention. The enzyme can be used to determine creatine in a sample by measuring the absorbance of a dye formed by reacting the sample with a reagent, comprising the enzyme, sarcosine oxidase and a composition for detecting hydrogen peroxide, e.g. for diagnosis of

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P-PSDB; AAW22893.
                                                                                                 Disclosure;
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02-MAR-1998
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                                                                                                                                                        Hattori T,
                                                                                                 Page 14-15;
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(first en
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/product= "Creatine_amidinohydrolase"
/product= "Creatine_amidinohydrolase"
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Best Local Sim
Matches 1211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uraemia, chronic nephritis, giantism and tonic muscular dystrophy. The enzyme has a lower Km value than prior art creatine amidinohydrolase (du 5451520). (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                         GTGCAATCCGGCGACATCCTTTCGCTCAACACCTTCCCGATGATCTTCGGCTACTACACC
                                                                                                                                     GTGCAATCCGGCGACATCCTTTCGCTCAACACCTTCCCGATGATCTTCGGGCTACTACACC
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 GACATCGCCATCGAGCTCAACGAGATGTACCGCGAGTGGGACCTGCTGAAGTACCGCTCC
                                                   GCGCTGGAGCGCACGCTGTTCTGCGACCATGTCGATGACGCCAGCCTCGACATCTGGGAG
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                                        AATGCGATGATCCGCGAGATCGCCAAATCGTTCCCCTTCGTGGAGCTGATGGACACCTGG
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Pred. No. 1.5e-195;
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Query Match Best Local

Similarity

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Score Pred. Ç

1210.4; DB 2; No. 1.5e-195;

1212

Sequence

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                                         This DNA encodes a stable creatine amidinohydrase which is a mutant creatine amidinohydrase and has improved long-term stability in a ne buffer compared to wild type creatine amidinohydrase. A recombinant plasmid containing the stable creatine amidinohydrase gene can be us transform a cell for the recombinant production of the enzyme. This stable creatine amidinohydrase is useful as a diagnostic agent can be produced commercially
                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                             New
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P-PSDB; AAW61905.
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/product= "A. faecalis creatine amidinohydrolase"
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The invention relates to Alcaligenes faecalis creatine amidinohydrolase, which catalyses creatine and water to sarcosine and urea. Creatine amidinohydrolase can be produced by culturing a microorganism producing the protein in a nutrient medium and recovering the protein from the resulting culture. Creatine amidinohydrolase is useful as a routine reagent for clinical tests for determining creatine and creatinine in biological samples. This is particularly useful in diagnosing diseases such as uraemia, chronic nephritis, acute nephritis, giantism and tonic muscular dystrophy. The presence of creatine in a sample can be determined by measuring an absorbance of a pigment produced by the reaction of a reagent containing creatine amidinohydrolase with the sample. This sequence represents genomic DNA encoding Alcaligenes Disclosure; Page 15-16; 21pp; English

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                                                            The invention relates to Alcaligenes faecalis TE3581 (FERM P-14237) creatineamidinohydrolase and the encoding gene. The gene can be used the commercial preparation of creatineamidinohydrolase. (Updated on 0 AUG-2003 to correct OS field.)
                                                                                                                                                     WPI; 2002-003140/01.
P-PSDB; AAM51471.
                                                                                                                                                                                                                                                                                                                                                                                         Alkaligenes
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28-JAN-2002
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                                                                                                              Claim 4; Page 10; 11pp; Japanese.
                                                                                                                                                                                                        16-MAY-1995;
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Query Match
Best Local Similarity
Matches 1211; Conserv
                                                                                                                                                 The present invention describes a stable mutant creatine amidinohydrase having a long-term stability in a neutral buffer solution. Also described are: (1) a creatine amidinohydrase gene encoding the above stable creatine amidinohydrase; (2) a gene encoding a mutant creatine amidinohydrase; (2) a gene encoding a mutant creatine compared to wild type creatine amidinohydrase, in which at least one gene among those found in a fully defined 1212 nucleotide sequence (the present sequence) is replaced by another gene; (3) a recombinant plasmid containing a gene encoding the above creatine amidinohydrase; (4) a cell transformed by the above plasmid; and (5) a method for the preparation of a stable creatine amidinohydrase in which the above cell is cultured in a medium and creatine amidinohydrase is collected. The creatine amidinohydrase is useful as a clinical diagnosing agent
                                                                                                           Sequence 1212
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term stability in a neutral buffer solution.
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Best Local S
Matches 1195
                                                                                                                                                                                                                                                                                                                                                CAH is used for quantification of creatine, e.g. to diagnose kidney disease by measuring creatine content of serum or urrine. CAH DNA can be inserted into host cells for the prodn. of CAH. CAH can now be produced efficiently without having to add creatine to the culture medium. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding creatine amidinohydrolase - useful creatine to, e.g. diagnose kidney disease.
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Erwinia; creatinase; creatine amidinohydrolase; enzyme; EC 3.5.3.3; Erwinia-type creatinase; creatine; creatinine; uraemia; gigantism; chronic nephritis; acute nephritis; tonic muscular dystrophy; gene; ds.
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New variant of an Erwinia-type creatinase modified relative to a wild-type creatinase having creatinase activity, useful for determining creatinine and/or creatine concentration in a sample.

Disclosure; Page 15-17; 51pp; English

The present invention describes a variant of an Erwinia-type creatinase (I) modified relative to a wild-type creatinase having creatinase activity. The variant comprises at least one amino acid substitution at a position of the fully defined 404 amino acid sequence given in ABR43467: these are selected from N130, M203, IZ78, I1304 and F395. Creatinase has the EC number EC 3.5.3.3 and is also known as creatine amidinohydrolase. Also described is a reagent (II) for determining creatine comprising the Erwinia-type creatinase variant. The variant is useful for determining creatinine and/or creatine concentration in a sample. Measuring creatinine and creatine are useful for diagnosing uraemia, chronic creatinine and creatine are useful for diagnosing uraemia, chronic nephritis, acute nephritis, gigantism, tonic muscular dystrophy and some other related diseases. The mutant enzymes have improved stability, lower conductivity and/or lower Km-values for creatine: they are much better suited to detection methods for creatine. The present sequence encodes Erwinia sp. (DSM 97-934) wild-type creatinase from the present invention 1215 BP; 242 A; 392 C; 358 ဂ္ 223 T; 0 U; 0 Other; lower

Query Match Best Local S Matches 1068 19 Н TTTTCGGATGCCGAGATGACCCGCCGCCAAAACGACGTTCGCGGCTGGATGGCCAAGAAC ATGACTGACGACATGTTGCACGTGATGAAATGGCACAACGGCGAGAAAGATTATTCGCCG ATGACTGACGACATGTTGCACGTGATGAAATGGCACAATGGTGAGAAGGAATATTCCCCC Conservative ٥, Mismatches 144; Indels 0; Gaps 120 60 60

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Similarity

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Score 981.6; DB 8; Pred. No. 6.5e-157;

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New variant of an Erwinia-type creatinase modified relative to a w type creatinase having creatinase activity, useful for determining creatinine and/or creatine concentration in a sample.

4; Page 33-35; 51pp; English.

The present invention describes a variant of an Erwinia-type creatinase (I) modified relative to a wild-type creatinase having creatinase activity. The variant comprises at least one amino acid substitution at a position of the fully defined 404 amino acid sequence given in AER43467: these are selected from N130, M203, I278, I1304 and F395. Creatinase has the EC number EC 3.5.3.3 and is also known as creatine amidinohydrolase. Also described is a reagent (II) for determining creatine amidinohydrolase. Erwinia-type creatinase variant. The variant is useful for determining creatinine and/or creatine are useful for dagnosing uraemia, chronic creatinine and creatine are useful for dagnosing uraemia, chronic creatinine, acute nephritis, gigantism, tonic muscular dystrophy and some other related diseases. The mutant enzymes have improved stability, lower conductivity and/or lower Km-values for creatine: they are much better suited to detection methods for creatine. The present sequence encodes a Erwinia creatinase from the present amidinohydrolase. ine comprising the lower

Sequence 1215 ВP; 241 A; 392 C; 361 G; 221 T; 0 Ç 0 Other;

Query Match Best Local Similarity Matches 1068; Conserv 81.0%; ilarity 88.1%; Conservative Score 981.6; DB 8; Pred. No. 6.5e-157; 0; Mismatches 144; Indels Length 0 Gaps 0

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chronic nephritis; acute nephritis; tonic muscular dystrophy; muta
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New variant of an Erwinia-type creatinase modified relative to a w-type creatinase having creatinase activity, useful for determining creatinine and/or creatine concentration in a sample.

Example 4; Page 20-21; 51pp; English.

The present invention describes a variant of an Erwinia-type creatinase (C) I) modified relative to a wild-type creatinase having creatinase (C) activity. The variant comprises at least one amino acid substitution at a CC position of the fully defined 404 amino acid sequence given in ABR43467: these are selected from N130, M203, I278, I1304 and F395. Creatinase has CC the EC number EC 3.5.3.3 and is also known as creatine comprising the EC Also described is a reagant (II) for determining creatine comprising the CC Erwinia-type creatinase variant. The variant is useful for determining CC creatinine and/or creatine concentration in a sample. Measuring CC creatinine and creatine are useful for diagnosing uraemia, chronic CC nephritis, acute nephritis, gigantism, tonic muscular dystrophy and some CC conductivity and/or lower Mr-values for creatine: they are much better conductivity and/or lower Mr-values for creatine. The present sequence encodes a cutant Erwinia creatinase from the present invention

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                                                                                                                                                                                          New variant of an Erwinia-type creatinase modified type creatinase having creatinase activity, useful creatinine and/or creatine concentration in a sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene;
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                                                                                                                                                                                                                                                                                   P-PSDB;
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/partial
/EC_number= "3.5.3.3"
/product= "creatinase mutant
/note= "no stop codon given"
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The present invention describes a variant of an Erwinia-type creatinase (I) modified relative to a wild-type creatinase having creatinase activity. The variant comprises at least one amino acid substitution at aposition of the fully defined 404 amino acid sequence given in ABR43467: these are selected from N130, M203, I278, I1304 and F395. Creatinase has the EC number EC 3.5.3.3 and is also known as creatine amidinohydrolase.

Example

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                                                                                                                                       GTGCAATCCGGCGACATCCTTTCGCTCAACACCTTCCCGATGATCTTCGGCTACTACACC
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                                      GCGCTGGAGCGAACGCTGTTCTGTGACCACGTCGACGATGCCAGCCTTGACACCTGGGAG
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Synthetic.
New variant of an Erwinia-type creatinase modified relative to a wild-type creatinase having creatinase activity, useful for determining creatinine and/or creatine concentration in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Erwinia; creatinase; creatine amidinohydrolase; enzyme; EC 3.5.3.3; Erwinia-type creatinase; creatine; creatinine; uraemia; gigantism; chronic nephritis; acute nephritis; tonic muscular dystrophy; mutant;
                                                                                          WPI; 2003-383834/37.
P-PSDB; ABR43475.
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The present invention describes a variant of an Erwinia-type creatinase CC (I) modified relative to a wild-type creatinase having creatinase activity. The variant comprises at least one amino acid substitution at a position of the fully defined 404 amino acid sequence given in ABR43467: these are selected from N130, M203, I278, I1304 and F395. Creatinase has CC these are selected from N130, M203, I278, I1304 and F395. Creatinase has CC the EC number EC 3.5.3.3 and is also known as creatine amidinohydrolase. CC Also described is a reagent (II) for determining creatine comprising the CC creatinine and/or creatinase variant. The variant is useful for determining CC creatinine and/or creatine concentration in a sample. Measuring CC creatinine and/or creatine are useful for diagnosing uraemia, chronic nephritis, acute nephritis, gigantism, tonic muscular dystrophy and some CO cher related diseases. The mutant enzymes have improved stability, lower conductivity and/or lower Xm-values for creatine; they are much better suited to detection methods for creatine. The present sequence encodes a cutant Erwinia creatinase from the present invention
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                       ACCTGGTTCCAGTCGGGCATCAACACCGACGGCGCGCACAATCCGGTCACCAACCGCATC
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Pred. No. 4.2e-15
0; Mismatches 14
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CC The present invention describes a variant of an Erwinia-type creatinase CC (I) modified relative to a wild-type creatinase having creatinase CC activity. The variant comprises at least one amino acid substitution at a CC position of the fully defined 404 amino acid sequence given in ABR43467; CC these are selected from N130, M203, IZ78, I1304 and F395. Creatinase has CC the EC number EC 3.5.3.3 and is also known as creatine amidinohydrolase. CC Also described is a reagent (II) for determining creatine comprising the CC Erwinia-type creatinase variant. The variant is useful for determining CC creatinine and/or creatine concentration in a sample. Measuring CC creatinine and creatine are useful for diagnosing uraemia, chronic CC comparist, acute nephritis, gigantism, tonic muscular dystrophy and some CC conductivity and/or lower Km-values for creatine; they are much better suited to detection methods for creatine. The present sequence encodes a CC mutant Erwinia creatinase from the present invention
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                                                 GCCTGCGCGGCTGCCATCAAGGCCGGCGTGCCCGAGCATGAAGTGGCGATCGCCACCA
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                              GCCTGCGTTGCCGCCGTCAAGGCCGGCGTTCCGGAGCACGAGGTCGCGATCGCCACAACC
                                                                                                 TCGCTCGAAGAGCAGAAGCTGATCCGCGAGGGTGCCCGTATCTGCGACGTCGGCGGTGCC
                                                                                                                  TCGCTCGAAGAGCAGAAGCTGATCCGCGAAGGCGCCCCGCGTGTGTGACGTCGGCGCGCG
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                                                                                                                                                                        Erwinia sp. Synthetic.
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                                                                                                                                                                                                                                                                                       Mutant Erwinia creatinase CTsd7 encoding
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                                                                                                                                                                                                                                               creatinase;
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                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a variant of an Erwinia-type creatinase (C (I) modified relative to a wild-type creatinase having creatinase c activity. The variant comprises at least one amino acid substitution at a position of the fully defined 404 amino acid sequence given in ABR43467: C these are selected from N130, M203, I278, I1304 and F395. Creatinase has the EC number EC 3.5.3.3 and is also known as creatine amidinohydrolase. CC Also described is a reagent (II) for determining creatine amidinohydrolase. CC Erwinia-type creatinase variant. The variant is useful for determining c creatinine and/or creatine concentration in a sample. Measuring CC creatinine and creatine are useful for diagnosing urasemia, chronic c nephritis, acute nephritis, gigantism, tonic muscular dystrophy and some CC conductivity and/or lower Km-values for creatine: they are much better CC suited to detection methods for creatine. The present sequence encodes a content Erwinia creatinase from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Sim:
Matches 1064;
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                                                 Erwinia sp. Synthetic.
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5
Erwinia; creatinase; creatine amidinohydrolase; enzyme; EC 3.5.3.3
Erwinia-type creatinase; creatine; creatinine; uraemia; gigantism;
chronic nephritis; acute nephritis; tonic muscular dystrophy; muta
                                                                     Mutant Erwinia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATGCGATGATCCGCGAGATCGCCAAATCGTTCCCCCTTCGTGGAGCTGATGGACACCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGTGATGTTGCCAGAAGGCGCTCCCGGCGCGCGGCGCCTACCGCGAGCACGACATCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGAACGTCGCCGTGCACCGCCGCGGCCTCGAACTCATCAAGCCGGGTGCGCGCTGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATGCGGTGGTCCGCGAGATCGCCAAGTCGTTCCCCTTCGTCGAACTGATGGACACCTGG
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                                                                                                      (first
                                                                     creatinase CTsd2
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                                    3.5.3.3;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a variant of an Erwinia-type creatinase (I) modified relative to a wild-type creatinase activity. The variant comprises at least one amino acid substitution at a position of the fully defined 404 amino acid sequence given in ABR43467: these are selected from N130, M203, I2798, I1304 and 2935. Creatinase has the EC number EC 35.3 and is also known as creatine amidinohydrolase. Also described is a reagent (II) for determining creatine comprising the Erwinia-type creatinase variant. The variant is useful for determining creatinine and/or creatine concentration in a sample. Measuring creatinine and/or creatine are useful for diagnosing uraemia, chronic nephritis, acute nephritis, gigantism, tonic muscular dystrophy and some other related diseases. The mutant enzymes have improved stability, lower conductivity and/or lower Km-values for creatine: they are much better sulted to detection methods for creatine. The present sequence encodes a mutant transfer for the present sequence encodes a
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 1063; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New variant of an Erwinia-type creatinase modified relative to a wild-type creatinase having creatinase activity, useful for determining creatinine and/or creatine concentration in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1212 BP; 239 A; 393 C; 360 G; 220 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example
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HOFFMANN LA ROCHE & CO AG
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ACCGACTGGCGCCGCGACAATTTCTATCGCGCCGTGCGCCAGCTGACCACGGGCGCCAAG
                                                              TCGGCCGGCATCGATGGCGGTCAGCCCTGGCGCCGTAGCTTCGGCGACAACATCACCTAT
                                                                                               TCGGCCGGCATCGACGGCGGCCAGCCTGGCGCGCAGCTTCGGCGACAACATCACCTAC
                                                                                                                            TACTGCTATTTCGGCCGCAAATACGGCATGGTCATCGACCAGGACCATGCCACGACCATC
                                                                                                                                              TACTGCTATTTCGGACGCAAGTACGGCATGGTCATCGACCACAACAACGACGACGACTT
                                                                                                                                                                                         GACGTCGACGCTGTTCACCTCCTATCATTGCATCAACTACTACTCTGGATTCCTG
                                                                                                                                                                                                          TTTTCCGATGCCGAGATGACGCGCCGCCAGAGTGACGTGCGGCGCTGGATGGCCGAAAAC
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/partial
/BC number= "3.5.3.3"
/product= "creatinase m
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                                                                                                                                                                                                                                                                                                                                                                              Score 973.6; DB 8; Pred. No. 1.5e-155; 0; Mismatches 149;
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120	CAGAAGGCGCT	1083	5 8
	ATGGTGATGCTGCCGGAGGGCATGCCCGGTGCCGGCGGCTATCGCGAGCACCGACATCCTG		y y
108	GCGAGGACATCGATACCGTGCTGCAGCCCGGCATGGTGGTCTCCATGGAG	1021	D D
108	GAGCTGCGCGAGGACATCGACACCGAGCTGAAGCCCCGGCATGGTGGTCGTCCATGGAGCCCG	1021	ρ
102	ceecer	961	밁
10	TTCGGCTATGGCCACTCCTTCGGCGTGCTGTGCCACTACTACGGTCGCGAGGCCGGCGTG	961	φ
96	GATATCGCCATCGAACTCAACGAGATGTACCGGGAGTGGGATCTGCTGAAGTACCGCTCC	901	밁
96	GACATCGC	901	Ş
90	AAGAACGTCGCCGTGCACCGCCGCGGCTCGAACTCATCAAGCCGGGTGCGCGCTGCAAG	841	рb
90	AAGAACGTGGCCGTGCATCGCCGCGGGCTCGAGCTGATCAAGCCGGGCGCGCGC	841	Ş
84	GCGCTGGAGCGAACGCTGTTCTGTGACCACGTCGACGATGCCAGCCTTGACACCCTGGGAG	781	당
84	GCGCTGGAG	781	Ş
78	GTGCAATCGGGCGATATCCTGTCGCTCAACACGTTCCCGATGATCTTCGGCTACTACACG	721	뮍
78	GIGCAAICCGGCGACAICCITICGCTCAACACCTTCCCGAIGAICTICIGGCTACIACA	721	S
72	. ACCTGGTTCCAGTCGGGCATCAACACCGACGGCGCCCACAATCCGGTGACCAACCGCATC	661	8
72	ACCTGGTTCCAGTCGGGCATCAACACCGACGGCGCGCACAATCCGGTCACCAACCGCA	661	Ş
66	AATGCGGTGGTCCGCGAGATCGCCAAGTCGTTCGCCCTTCGTCGAACTGATGGACACCTC	601	뮍
99	AATGCGATGATCCGCGAGATCGCCAAATCGTTCCCCCTTCGTGGAGCTGATGGACACCT	601	Ş
60	GCCTGCGTTGCCGCCGTCAAGGCCGGCGTTCCCGGAGCACGAGGTCGCGATCGCCACAACC	541	망
60	GCCTGCGCGGCTGCCATCAAGGCCGGCGTGCCCGAGCATGAAGTGGCGATCGCCACCA	541	Ş
54	TCGCTCGAAGAGCAGAAGCTGATCCGCGAGGGTGCCCGTATCTGCGACGTCGGCGGTGCC	48:	ם
54	GCTCGAAGAGCAGAAGCTGATCCGCGAAGGCGCCCGCGTGTGTGGACGTCGGCGGCG	481	Ş
4.8	CTGCCCGGCGTCGAGTTCGTCGATATCGGTCAACCGTCGATGTGGATGCGCACGGTCAAG	42:	дb
48	CTACCGGGCGTCGACTTCGTCGACATCAGCCAGCCCTCGATGTGGATGCGCACCATCA	421	Ş
42	CGCATCGGTATCGAGTTCGATCACGTGGACCTTGACTTCCGCCGCACGCTCGAAGAGGGCG	. 36:	D
42	CGCATCGGCATCGAGTTCGACCACGTCAATCTCGACTTCCGCCCGC	36:	δ

Search completed: November 19, 2004, 16:39:06 Job time: 664 Becs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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1: /cgn2_6/pcodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Gapop 10.0 , Gapext 1.0
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1212
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                              1056
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US-947-781-1
US-09-252-991A-4435
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US-08-393-0022A-1
US-08-343-428-1
US-09-475-515-54
US-09-475-515-56
US-09-475-515-64
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US-09-475-515-64
US-09-475-615-73
US-09-266-965-66
US-09-266-965-76
US-09-266-991A-1566
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•	•	-	Sequence 26, Appl	•	Sequence 26, Appl	e 17,	Sequence 26, Appl	•	e 26,	e 17,		e 24,	•	•	e 24,	Sequence 24, Appl	•

ALIGNMENTS

TELEFAX: (312) 616-5700 TELEX: 25-353 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS: LENGTH: 1212 base pairs NAME: Robert F. Green REGISTRATION NUMBER: 27555 REFERENCE/DOCKET NUMBER: 7806 TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 616-5600 TELEFAX: (312) 616-5700 MOLECULE TYPE: 9 ORIGINAL SOURCE: ORGANISM: Alca ZIP: 60601-6780 COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #10, Version #1.25 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/799,897 FILING DATE: 13-FEB-1997 CLASSIFICATION: 435 PRIOR APPLICATION UMBER: JP 25435/1996 FILING DATE: 13-FEB-1996 ATTORNEY/AGENT INFORMATION: APPLICATION TORNER: JP 25435/1996 ATTORNEY/AGENT INFORMATION: APPLICANT: Hattori, Takashi APPLICANT: Nishiya, Yoshiaki APPLICANT: Kawamura, Yoshihisa TITLE OF INVENTION: NOVEL CREATINE AMIDINOHYDROLASE, PRODUCTION TITLE OF INVENTION: THEREOF AND USE THEREOF NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS STRANDEDNESS: TOPOLOGY: lir TYPE: nucleic acid ADDRESSEE: LEYDIG, VOIT & MAYER, LTD. STREET: Two Prudential Plaza, Suite 4900 INFORMATION: Chicago : Illinois Application US/08799897 : Alcaligenes faecalis TE3581 (FERM P-14237) Sogabe, Atsushi linear genomic DNA double 27555 78064

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TTCGGCTATGGCCACTCCTTCGGCGTGCTGTGCCACTACTACGGTCGCGAGGCCGGCGTG 1020
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                    GACATCGCCATCGAGCTCAACGAGATGTACCGCGAGTGGGACCTGCTGAAGTACCGCTCC
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Pred. No. 5.1e-255;
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APPLICATION UNMBER: US/08/947,726A
FILING DATE: 09-OCT-1997
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/535,444
FILING DATE: 27-SEP-1995
PRIOR APPLICATION NUMBER: UP 94/235737
FILING DATE: 29-SEP-1994
APPLICATION NUMBER: UP 94/235737
FILING DATE: 29-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence III, Stanton T.
REGISTRATION NUMBER: 25,736
REGISTRATION INFORMATION:
TELEPHONE: (212) 790-9090
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 869-9741
                                                                                                                                                                                                 TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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MOLECULE TYPE: D. ORIGINAL SOURCE: ORGANISM: Alca STRAIN: FERM B
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APPLICANT: Ichikawa, Toshio
APPLICANT: Suzuki, Marsari
APPLICANT: Suzuki, Marsari
APPLICANT: Koyama, Yasuji
TITLE OF INVENTION: A NOVEL CREATINE AMIDINOHYDROLASE GENE,
TITLE OF INVENTION: CREATINE AMIDINOHYDROLASE
TITLE OF INVENTION: CREATINE AMIDINOHYDROLASE
TITLE OF SEQUENCES: 5
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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TTCGGCTATGGCCACTCCTTCGGCGTGCTGTGCCACTACGGTCGCGAGGCCGAGGCGTG
                                                               GACATCGCCATCGAGCTCAACGAGATGTACCGCGAGTGGGACCTGCTGAAGTACCGCTCC
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GENERAL INCORNATION:
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO P
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4171
LENGTH: 858
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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 GCGCTGCAAGGACATCGCCATCGAGCTCAACGAGATGTACCGCGAGTGGGACCTGCTGAA
                         CCTCTGCCAGATCACCCAGGAATGCATGTACAAGGGCATTTCCGTGGTGCGTCCGGGCGC
                                                CATCTGGGAGAAGAACGTGGCCGTGCATCGCCGCGGCTCGAGCTGATCAAGCCGGGCGC
                                                                         CTACCACGGCGACACCAGCAAGATGTTCCTGGTCGGCAAGACCCCGGAATGGGCCGACCG
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APPLICANT: MATC J. Rubenfield et al.

APPLICANT: MATC J. RUBENFIELD AND AMINO ACID SEQUENCES RELATING TO F
ITITE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO F
ITITE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NO 435
LENGTH: 963
TYPE: DNA
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US-09-252-991A-4435/c
; Sequence 4435, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
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  CCTCTGCCAGATCACCCAGGAATGCATGTACAAGGGCATTTCCGTGGTGCGTCCGGGCGC
                                    CATCTGGGAGAAGAACGTGGCCGTGCATCGCCGCGGGCTCGAGCTGATCAAGCCGGGCGC
                                                                           CTACCACGCGACACCAGCAAGATGTTCCTGGTCGGCAAGACCCCGGAATGGGCCGACCG
                                                                                                               CTACTACACCGCGCTGGAGCGCACGCTGTTCTGCGACCATGTCGATGACGCCAGCCTCGA
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Pred. No. 2.5e-07;
0; Mismatches 360
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4314
LENGTH: 1176
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US-09-252-991A-4314
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APPLICANT: Marc J.
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107195.136
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                                                                           CTACTACACCGCGCTGGAGCGCACGCTGTTCTGCGACCATGTCGATGACGCCAGCCTCGA
                                                                                                                  CGAGAAGCCGCTGAAGGAAGGCGACATCCTCAACGTCGACATCACCGTCATCAAGGACGG
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                                                                                                                                                                                                                               GGACACCTGGACCTGGTTCCAGTCGGGCATCAACACCGACGCGCGCACAATCCGGTCAC 710
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Pred. No. 2.6e-07;
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RESULT 6
US-08-939-002A-1
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 221193/1997
APPLICATION NUMBER: JP 221193/1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 8361-001-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT: HAYASHI
APPLICANT: LIU, AII
APPLICANT: LI, HEB
APPLICANT: HARAGUC
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                                                                                                                                                                                  TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LI, HEBIAO
APPLICANT: HARAGUCHI, KAZUTOMO
APPLICANT: HARAGUCHI, KAZUTOMO
APPLICANT: KITAWURA, YOSHIAKI
TITLE OF INVENTION: CELLOBIOSE PHOSPHORYLASE GENE, VECTOR
TITLE OF INVENTION: AND TRANSFORMANT CONTAINING SAID GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/939,002A
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                                                                                  TOPOLOGY:
                                                                                                        STRANDEDNESS:
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LOCATION: 359.2824

OTHER INFORMATION: /note= "METHOD FO!

OTHER INFORMATION: SEQUENCE: E"

FEATURE:

NAME/KEY: CDS
LOCATION: 359.2824

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Pred. No. 3.3e-05;
0; Mismatches 597;
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RESULT 7
US-08-343-428-1
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APPLICANT: Nakamu
                                                                                                                                                                                                                                                                TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 18-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/J93/00592
FILING DATE: 30-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: .WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,428
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ADDRESSEE: James F. Haley,
STREET: 1251 Avenue of the
                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: SI
TELECOMMUNICATION INFORMATION:
                IDENTIFICATION FINENCE CDS
                                                                                                                                            FEATURE:
                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                              STRANDEDNESS:
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FILING DATE: 19-MAY-1992
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OPERATING SYSTEM:
                                                                                                                                                             ORGANISM:
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                                                                        NAME/KEY:
                                                                                      LOCATION: 359..364
IDENTIFICATION METHOD:
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INVENTION: No. 5665586el Protease
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Tsuzuki, Hiroshige
Kitadokoro, Kengo
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Sequence 2, Application US/0902001
Patent No. 6069299
GENERAL INFORMATION:
APPLICANT: Broadway, Roxanne M.
APPLICANT: Harman, Gary E.
APPLICANT: Harman, Gary E.
TITLE OF INVENTION: FUNGUS AND INSECT CONTROL WITH
TITLE OF INVENTION: CHITINOLYTIC ENZYMES
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Best Local Similarity
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NAME/KEY: 81g peptide
LOCATION: 435..944
IDENTIFICATION METHOD:
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Pred. No. 5.5e-
0; Mismatches
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TELEPAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1294 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
09-025-691-2
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Best Local Similarity 42.5%;
Matches 389; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPOSIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: CILL
STREET: Nochester
CITY: Rochester
STATE: New York
"1 S.A.
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REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19:
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                           GCAATCCGGCGACATCCTTTCGCTCAACACCTTCCCGATGATCTTCGGCTACTACACCGC
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Pred. No. 9.1e-05;
0; Mismatches 523;
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TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLITIFIE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PATENTIN VEY. 2.0
SEQ ID NO 54
LENGTH: 1599
TYPE: DNA
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; OTHER INFORMATION: Description
US-09-475-515-54
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                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local &
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APPLICANT: BARNETT, Susan
APPLICANT: ZUR MEGEDE
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Sequence 56, Application US/09475515A

Patent No. 6602705

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BARNETT, SUBAN
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: GREER, Catherine
APPLICANT: GREER, Catherine
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF
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; FILE REFERENCE: 1621.002
; CURRENT APPLICATION NUMBER: US/09/475,515A
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patentin Ver. 2.0
; SOFTWARE: Patentin Ver. 2.0
; SOFTWARE: DNA
; ORGANISM: Artificial Sequence
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Pred. No. 0.00025;
0; Mismatches 579;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 57
LENGTH: 2112
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Matches 434; Conserv
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Patent No. 6602705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LIU, Hong
APPLICANT: GREER, Catherine
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BARNETT, Susan
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
OTHER INFORMATION:
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 GCCATCAAGGCCGGCGTGCCCGAGCATGAAGTGGCGATCGCCACCACCAATGCGATGATC
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                              TGCCCCAAGGTGAGCTTCGAGCCCATCCCCATCCACTACTGCGCCCCCCGCCGGCTTCGCC
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Pred. No. 0.00025;
0; Mismatches 579;
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GAGGTGGGCAAGGCCATGTACGCCCCCCCCCATCCGCGCCAGATCAAGTGCAGCAGCAA 1379
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US-09-475-515-58

Sequence 58, Application US/09475515A

Patent No. 6602705

GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: TZUR MEGEDE, Jan
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: GREER, Catherine
APPLICANT: SELBY, Mark
APPLICANT: MALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT APPLICATION STEEL 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 58
LENGTH: 2181
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: gpl40TM.modUS4
US-09-475-515-58
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                                               GACGGTGCCGAGAACATCACCGGCTTCCCGTTCGGTCCGGAACACACCATCATCCGCAA 1211
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Pred. No. 0.00025;
0; Mismatches 579;
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APPLICANT: HARTOG, Karin
APPLICANT: HARTOG, Karin
APPLICANT: LIU, Hong
APPLICANT: GREER, Catherine
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REPERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 64
LENGTH: 2634
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; Sequence 64, Application
; Patent No. 6602705
; GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
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ORGANISM: Artificial Sequence
FEATURE:
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ATCGTGCAGCTGAACGAGTCCGTGGAGATCAACTGCATCCGCCCCAACAACAACACGCGT
                               GACATCCTTTCGCTCAACACCTTCCCGATGATCTTCGGCTACTACACCGCGCTGGAGCGC
                                                                                                TCGGGCATCAACACCGACGGCGCGCACAATCCGGTCACCAACCGCATCGTGCAATCCGGC
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Pred. No. 0.00026;
0; Mismatches 579;
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APPLICANT: GREER, Catherine
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POI
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
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US-09-475-515-73
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No. 6602705
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APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: HARTOG, Karin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0 EQ ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial OTHER INFORMATION: gp160.modUS4.gag.modSF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                            5.0%; Score 60.6; DB 4;
42.6%; Pred. No. 0.00029;
tive 0; Mismatches 579
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                                                                                                                             Sequence 4, Application US/09025691
Patent No. 6069299
GENERAL INFORMATION:
APPLICANT: Broadway, Roxanne M.
APPLICANT: Harman, Gary E.
TITLE OF INVENTION: CHITINOLYTIC ENZYMES
                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargri
STREET: Clinton Square,
CITY: Rochester
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                                                  Hargrave,
                           P.O.
                           Devans & Doyle LLP . Box 1051
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STATE: New York COUNTRY: U.S.A. ZIP: 14603

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2712 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 4.9%;
Best Local Similarity 43.2%;
Matches 394; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLdman, Michael L.
REGISTRATION UMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/20120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025 CCLASSIPTOTE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                     1745
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ATGATCTTCGGCTACTACACCGCGCTGGAGCGCACGCTGTTCTGCGACCATGTCGATGAC 819
                                   GAGTCGGTCGACGCCGTCGCCGACACCTGGGACCAGCCGCTGCGCGGCAACTTCAACCAG
                                                                         AATCCGGTCACCAACCGCATCGTGCAATCCGGCGACATCCTTTCGCTCAACACCTTCCCG
                                                                                                                 GGCGGCAAGTGCACCATCGGTGACAGCTTCGCCGCCTACGACAAGGCGTACACCGCCGCC 1744
                                                                                                                                            CTGATGGA-----CACCTGGACCTGGTTCCAGTCGGGCATCAACACCGACGGCGCGCAC
                                                                                                                                                                                        GTGACCTCCGGCTCCGCCGAGAGATCACCCCACATCAACTACTCCTTCGGCAACGTCCAG
                                                                                                                                                                                                                            GCGATCGCCACCAATGCGATGATCCGCGAGATCGCCAAATCGTTCCCCTTCGTGGAG
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Pred. No. 0.00043;
0; Mismatches 509; Indels
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2105 GACGCCAGCTCC
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                                   1060 ATGGTGGTCTCC 1071
                                                                        2045 ATGGTCCAGGCGATGCGCGCCCAGTTCGGCACCGGCTGGTCACCGCCGCCATCACCGCC 2104
                                                                                                   1000 TACGGTCGCGAGGCCGGGGTGGAGCTGCGCGAGGAGCACCGAGCTGAAGCCCGGC 1059
                                                                                                                                                1985 GAGTACCCGAACGCCTGCGGCCTCAGCTGCGACAGCTCCGGTCCGGCCGCGCTGAAGAAC
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Search completed: November 19, 2004, 14:49:17 Job time : 128 secs

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Maximum DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0% Maximum Match 100%
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seq length: 2000000000
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Match Length
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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US-10-251-078-15

US-10-251-078-19

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                                                   Sequence 1, Appli
Sequence 17, Appli
Sequence 9, Appli
Sequence 11, Appl
Sequence 13, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 88003, A
Sequence 109294,
Sequence 38426, A
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US-10-156-761-7186	US-09-748-033-2	-10-411-910A-20	US-10-156-761-4461	-10-411-910A-26	-10-359-120-	-10-156-761-	US-10-156-761-15103	-10-156-761-	-10-260-238-27	-10-463-6	-10-411-910A-	-10-411-910A-	-10-081-864-1	US-10-006-9	US-10-473-687-	US-10-437-963-2936	US-10-437-	US-10-411-910A-23	US-10-437-963-	US-10-282-1	US-10-437-963-	US-10-156-761-393	US-10-228-063-	US-10-282-122A-	US-10-156	US-10-156-761-2	US-10-437-963-8	US-10-411-910A-	US-10-156-761-4932	US-10-437-963-5	US-10-203-295-35	0-203-295-
Sequence 7186, Ap	Sequence 2, Appli	e 209	e 446:	e 266	e 176	5241,	e 151	412	9 271	ø	e 200	e 220	e 19,	e 27,	e 3,	e 293	e 343	æ	9 112, Ap	Sequence 11731, A	322	equence 393	e 48, 7	246	Ce 1,	e 2222, Ap	e 8800	e 222,	O	e 5701	5, App	Sequence 1, Appli

ALIGNMENTS

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APPLICANT: Roche Diagnostics GmbH
APPLICANT: Shao, Zhixin
APPLICANT: Shao, Zhixin
APPLICANT: Schmuck, Rainer
APPLICANT: Schmuck, Rainer
APPLICANT: Kratzsch, Peter
APPLICANT: Weisser, Harald
ITILE OF INVENTION: Variants of an Erwinia-type creatinase
FILE REFERENCE: 20981 EP
CURRENT APPLICATION NUMBER: US/10/251,078
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1215
TYPE: DNA
ORGANISM: Erwinia sp.
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; NAME/KEY: CDS
; LOCATION: (1)..(1215)
US-10-251-078-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10251078
Publication No. US20030119084A1
GENERAL INFORMATION:
                                                                                                                                         Query Match 81.0%;
Best Local Similarity 88.1%;
                                                                                                                        Matches 1068;
    61 TTTTCGGATGCCGAGATGACCCGCCGCCAAAACGACGTTCGCGGCTGGATGGCCAAGAAC 120
                                                             ATGACTGACGACATGTTGCACGTGATGAAATGGCACAACGGCGAGAAAGATTATTCGCCG
                                                                                                                        Conservative
                                                                                                                    Score 981.6; DB 15;
Pred. No. 8.9e-254;
0; Mismatches 144;
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; TYPE: DNA;
; ORGANISM: Artificial Sequence;
; FEATURE:
; PEATURE:
; PEATURE:
; NAME/KEY: CDS;
; LOCATION: (1)..(1215)
US-10-251-078-17
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US-10-251-078-17
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CURRENT APPLICATION NUMBER: US/10/251,078
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 17
LENGTH: 1215
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Publication No. US20030119084A1
GENERAL INFORMATION:
APPLICANT: Roche Diagnostics GmbH
APPLICANT: Shao, Zhixin
APPLICANT: Schmuck, Rainer
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Best Local Similarity 88.1%;
Matches 1068; Conservative
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APPLICANT: Kenklies, Janet
APPLICANT: Weisser, Harald
TITLE OF INVENTION: Variants of an Erwinia-type
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Pred. No. 8.9e-254;
0; Mismatches 144;
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US-10-251-078-9

Sequence 9, Application US/10251078

Publication No. US20030119084A1

GENERAL INFORMATION:
APPLICANT: Schauck, Rainer
APPLICANT: Schauck, Rainer
APPLICANT: Kenklies, Janet
APPLICANT: Kenklies, Janet
APPLICANT: Weisser, Harald

TITLE OF INVESTION: Variants of an Erwinia-type cre
FILE REFERENCE: 20981 EP
CURRENT APPLICATION NUMBER: US/10/251,078

CURRENT FILING DATE: 2002-09-20

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn version 3.1

SEQ ID NO 9

LENGTH: 1215

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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US-10-251-078-9
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Similarity 88.0%;
66; Conservative
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                                     GATATCGCCATCGAACTCAACGAGATGTACCGGGAGTGGGATCTGCTGAAGTACCGCTCC
                                                                                   GCGCTGGAGCGCACGCTGTTCTGCGACCATGTCGATGACGCCAGCCTCGACATCTGGGAG
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Pred. No. 6.5e-253;
0; Mismatches 146;
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; OTHER INFORMATION: Description: pearTure:
; NAME/KEY: CDS
; LOCATION: (1)..(1212)
US-10-251-078-11
                                                                                                                                                                                                                                                                                                                               Sequence 11, Application US/10251078
Publication No. US20030119084A1
GENERAL INFORMATION:
APPLICANT: Roche Diagnostics GmbH
APPLICANT: Schmuck, Rainer
APPLICANT: Schmuck, Rainer
APPLICANT: Kratzsch, Peter
APPLICANT: Kratzsch, Peter
APPLICANT: Kenklies, Janet
APPLICANT: Kenklies, Janet
APPLICANT: Kenslies, Janet
APPLICANT: Weisser, Harald
TITLE OF INVENTION: Variants of an Erwinia-t
FILE REFERENCE: 20981 EP
CURRENT APPLICATION UNUMBER: US/10/251,078
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
LENGTH: 1212
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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FORMATION: Description of Artificials
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Pred. No. 1.7e-252;
O; Mismatches 147;
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RESULT 5
US-10-251-078-13
; Sequence 13, Application US/10251078
; Publication No. US20030119084A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; APPLICANT: Shao, Zhixin
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APPLICANT: Schmuck, Rainer
APPLICANT: Kratzsch, Peter
APPLICANT: Kratzsch, Peter
APPLICANT: Weisser, Harald
TITLE OF INVENTION: Variants of an Erwinia-type cre
FILE REFERENCE; 20981 EP
CURRENT APPLICATION NUMBER: US/10/251,078
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ.ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
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; NAME/KEY: CDS
; LOCATION: (1)..(1212)
US-10-251-078-13
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Best Local Similarity . 87.9%;
Matches 1065; Conservative
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TYPE: DNA
ORGANISM: Artificial Sequence
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Pred. No. 1.7e-252;
0; Mismatches 147;
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APPLICANT: Shao, Zhixin

APPLICANT: Schmuck, Rainer

APPLICANT: Kratzsch, Peter

APPLICANT: Kenklies, Janet

APPLICANT: Weisser, Harald

TITLE OF INVENTION: Variants of an Erwinia-t

FILE REFERENCE: 20981 EP

CURRENT APPLICATION NUMBER: US/10/251,078

CURRENT FILING DATE: 2002-09-20

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin version 3.1

SEQ ID NO 15

LENGTH: 1215
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                                                                                              ; NAME/KEY: CDS
; LOCATION: (1)..(1215)
US-10-251-078-15
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US-10-251-078-15
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                                            Query Match
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Matches 1065
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                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Roche Diagnostics APPLICANT: Shao, Zhixin
                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description
FEATURE:
FEATURE:
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                                             Score 976.8; DB 15;
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0; Mismatches 147;
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APPLICANT: Kratzsch, Peter
APPLICANT: Kenklies, Janet
APPLICANT: Weisser, Harald
TITLE OF INVENTION: Variants of an Erwinia-t
FILE REFERENCE: 20981 EP
CURRENT APPLICATION NUMBER: US/10/251,078
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 1212
TYPE: DNA
ORGANISM: Artificial Sequence
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Publication No. US20030119084A1
GENERAL INFORMATION:
APPLICANT: Roche Diagnostics GmbH
APPLICANT: Shao, Zhixin
APPLICANT: Schmuck, Rainer
APPLICANT: Kratzsch, Peter
APPLICANT: Kratzsch, Janet
APPLICANT: Kenklies, Janet
APPLICANT: Weisser, Harald
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Best Local Similarity 87.8%;
Matches 1064; Conservative
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OTHER INFORMATION:
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Pred. No. 4.7e-252;
0; Mismatches 148;
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Sequence 19, Application US/10251078

Publication No. US20030119084A1

GENERAL INFORMATION:
APPLICANT: Sche Diagnostics GmbH
APPLICANT: Shao, Zhixin
APPLICANT: Shao, Zhixin
APPLICANT: Schmuck, Rainer
APPLICANT: Kratzsch, Peter
APPLICANT: Kratzsch, Peter
APPLICANT: Weisser, Harald
TITLE OF INVENTION: Variants of an Erwinia-type cre
FILE REFERENCE: 20981 EP
CURRENT APPLICATION NUMBER: US/10/251,078
CURRENT FILING DATE: 2002-09-20
INUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 1212
TYPE: DNA
ORGANISM: Artificial Sequence
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Similarity 87.7%;
63; Conservative
       GACATCGCCATCGAGCTCAACGAGATGTACCGCGAGTGGGACCTGCTGAAGTACCGCTCC
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Pred. No. 1.3e-251;
0; Mismatches 149;
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360 360 360 420

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APPLICANT: Barbazuk, Brad
APPLICANT: L1, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 88003
LENGTH: 2733
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE
FEATURE
FEATURE
TIFORMATION: Clone ID: PAT_MRT4530_86897C.1
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US-10-437-963-88003/c
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Best Local Similarity
Matches 399; Conserv
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
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CAAGGACGTGGCCGACGGCGGCGGGAAGTGGTGGGGCGCGGCGTCGGCGACGCGGC
                                                               CCTCGGCGACGACAAGAAGAAGCTCCCCCACGGTCCGACCATCCACGTCCGGCTGCAGTT
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Cao, Yor
Wu, Wei
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Barbazuk, Brad
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Pred. No. 3.8e-10;
0; Mismatches 491;
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US-10-425-115-109294/c
US-10-425-115-109294, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
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                                                                               Query Match
Best Local S
Matches 308
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SEQ ID NO 109294
LENGTH: 1262
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecule:
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                               hes 308;
               1107
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                                                                             h 6.1%;
Similarity 44.1%;
08; Conservative
               GGCAGCGGCCTCCCGTCCAAGAGCGACGTGGTGCAGCTCTACAAGTCCAACGGCATCGCC
                                             GGACATCGACACCGAGCTGAAGCCCGGGCATGGTGTCTCCATGGAGCCGATG---GTGAT 1088
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                                                                                                                                                              Clone ID: MRT4577_31174C.1
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Pred. No. 1.2e-09;
0; Mismatches 391;
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APPLICANT:
APPLICANT:
                                                                                        APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 38426

LENGTH: 1483
                                                                                                                                                                                                                                                                                  APPLICANT:
                                       OTHER INFORMATION: Clone
                                                      FEATURE:
                                                                ORGANISM: Oryza
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Kovalic, David
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Barbazuk, Brad
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Best Local Similarity Matches 266; Conserv
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Sequence 1, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: ONURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
ORGANISM: Streptomyces a FEATURE: NAME/KEY: misc_feature LOCATION: (4187715)
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILLING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                NUMBER OF SEQ ID NOS: 15109
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HORIKAWA, HIROSHI
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Query Match

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RESULT 13
US-10-203-295-1
J Sequence 1, Application US/10203295
Publication No. US20040115762A1
GENERAL INFORMATION:
APPLICANT: Zotchev, Sergey Borisov.
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Pred. No. 5.8e-08;
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US-10-203-295-1
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PRIOR FILING DATE: 2001-02-08
PRIOR PPLICATION NUMBER: GB 0002840.7
PRIOR PILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: GB 0008786.6
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
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Best Local Similarity 42.8%;
Matches 404; Conservative
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CURRENT FILING DATE: 2003-05-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 65140
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GENERAL INFORMATION:
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CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: PCT/GB 01/00509
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: GB 0002840.7
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: GB 0008786.6
PRIOR APPLICATION NUMBER: GB 0008786.6
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 35
LENGTH: 125401
TYPE: DNA
ORGANISM: Streptomyces noursei ATCC 11455
S-10-203-295-35
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APPLICANT: Strom, Arne Reidar
APPLICANT: Valla, Svein
APPLICANT: Valla, Svein
APPLICANT: Ellingsen, Trond Erling
APPLICANT: Sletta, Havard
APPLICANT: Gulliksen, Ole-Martin
TITLE OF INVENTION: Movel genes encoding a nystatin polyketide synthase
TITLE OF INVENTION: manipulation and utility
FILE REFERENCE: 1181-265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Zotchev, Sergey Borisovich
APPLICANT: Sekurova, Olga Nikalayivna
APPLICANT: Fjaervik, Epsen
APPLICANT: Brautaset, Trygve
APPLICANT: Strom, Arne Reidar
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Pred. No. 4.5e-08;
0; Mismatches 537;
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US-10-437-963-57011/c
US-10-437-963-57011, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
           APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
       CURRENT APPLICATION NUMBER: US/10/437,963
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NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 57011
LENGTH: 1169
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_58865C.1
US-10-437-963-57011
Search completed: November 19,
Job time : 692 secs
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                                                                                                 1072 АТССАСС 1078
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                                                                                                                                                                                                                                                                                                                                                                   ATCTGGGAGAAGAAGGTGGCCGTGCATCGCCGCGGGCTGAGCTGATCAAGCCGGGCGCG 891
                                                                                                                                   ACCGACGTGCCGACGTACGTGATGTTCTACGACGAGCAGGCGGCGAACTACCCGGGCGGC 379
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                                                                 AAGGTGC 372
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Maximum DB
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Perfect score:
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(without alignments)
10869.546 Million cell updates/sec
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  GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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AX928133 Sequence	AX928131 Sequence	AP003011 Mesorhizo	Continuation (5 of	AL939126 Streptomy	AL939128 Streptomy			AF271357 Oryza sat	AK119861 Oryza sat	AE016921 Chromobac	AL939111 Streptomy	AL939105 Streptomy	AE017230 Mycobacte	E17219 gDNA encodi	AB007122 Arthrobac	D14463 Bacillus sp	E01828 Genomic DNA	E01576 DNA sequenc	AF072304 Pseudomon	AF170566 Pseudomon	AE016787 Pseudomon	A01506 Recombinant		E00904 gDNA encodi	A10619 Recombinant

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					/mol_type="unassigned DNA"	/mo1_t	
					/organism="unknown"	/organ	
					12		source
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			mura, Y.	d Kawai	Sogabe, A., Hattori, T., Nishiya, Y. and Kawamura, Y.	Sogabe, A., Hatt	AUTHORS
					1212)	1 (bases 1 to 1212)	REFERENCE
						Unclassified.	
						Unknown.	ORGANISM
						Unknown.	SOURCE
						•	KEYWORDS
					12810570	AR100122.1 GI:12810570	VERSION
						AR100122	ACCESSION
					Sequence 2 from patent US 6080553.	Sequence 2 from	DEFINITION
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Best Local Similarity
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1 (Dasses | to 1212)

SOGADE, A., YAMAMOTO, K. and Kawamura, Y.
SOGADE, A., YAMAMOTO, K. and Kawamura, Y.
SOGADE, A., YAMAMOTO, K. and Kawamura, Y.
SOGADE ATTENERS |

PATENT: JP 1996308579-A 1 26-NOV-1996;

TOYOBO CO LTD

OS Alcaligenes faecalis
PN JP 1996308579-A/1

PD 26-NOV-1996

PF 16-MAY-1995 JP 1995117283

PI 8-MAY-1995 JP 1995117283

PI 8-MAY-1995 JP 1995117283

PI SOGABE ATSUSHI, YAMAMOTO KAZUMI, KAWA C12N15/09,C12N1/21,C12N9/78,(C12N15/09,C12 C12R1:425);

PC C12N15/09,C12N1/21,C12N9/78,(C12N15/09,C12 C12R1:425);

PC (C12N9/78,C12R1:425);

PC strandedness: Double;

CC strandedness: Double;

CC strandedness: No;
CC anti-sense: No;
CC anti-sense: No;
FH Key

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Alcaligenaceae; Alcaligenes.
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                         CTACCGGGCGTCGACTTCGTCGACATCAGCCAGCCCTCGATGTGGATGCGCACCATCAAG
                                                          ACCGACTGGCGCCGACAATTTCTATCGCGCCGTGCGCCAGCTGACCACGGGCGCCAAG
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JP 1996308579-A/1

26-NOV-1996

16-MAY-1995 JP 1995117283

F 16-MAY-1995 JP 1995117283
F SCGABE ATSUSHI, YAMAMOTO KAZUMI, KAWAMURA YOSHIHISA PC 12N15/09,C12R1:05),(C12N1/21,C12N15/09,C12R1:05),(C12N1/21,C12R1:425),
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amidinohydrolase'.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:511"
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Alcaligenes faecalis gene for creatine amidinohydy
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E13584.1 GI:3252389

JP 1997215494-A/1.

Alcaligenes faecalis
Alcaligenes faecalis
Bacteria; Proteobacteria; Betaproteobacteria; Burl
Alcaligenes en co 1212)
Sogabe,A., Hattori,T., Nishiya,Y. and Kawamura,Y.
NEW CREATINE AMIDINOHYDOLASE, ITS PRODUCTION AND
Patent: JP 1997215494-A/1
PD 19-AUG-1997
PF 13-FEB-1996 JP 1996025435
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                                                                   Burkholderiales;
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         GTGCAATCCGGCGACATCCTTTCGCTCAACACCTTCCCGATGATCTTCGGCTACTACACC
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Query Match
Best Local Similarity
Matches 1211; Conser
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PC C12N9/78,C12N15/09,(C12N9/78,C12R1:05),(C12N15/09,C12R1:19);
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH FH source 1..1212
FT source 1..1212
FT source 1..1212
                                                                                                                                   ACCTGGTTCCAGTCGGGCATCAACACCGACGGCGCGCACAATCCGGTCACCAACCGCATC
                                                                                  AATGCGATGATCCGCGAGATCGCCAAATCGTTCCCCTTCGTGGAGCTGATGGACACCTGG
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/mol_type="genomic DNA"
/db_xref="taxon:511"
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Pred. No. 2.6e-145;
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El (bases 1 to 1212)

RS Sogabe, A., Nishiya, Y. and Kawamura, Y.

STABLE CREATINE AMIDINOHYDROLASE

PAtent: JP 1998174585-A 1 30-JUN-1998;

TOYOBO CO LTD

OS Alcaligenes faecalis
PN JP-1998174585-A/1

PD 30-JUN-1998
PT 17-DEC-1996 JP 1996337027
PI SOGABE ATSUSHI, NISHIYA YOSHIAKI, KAWAMURA YOSHIHISA PC C12N9/78, C07H21/04, C12N1/21, C12N15/09//C12Q1/34, (C12N9/78, PC C12N1/21, C12N1/21, C12N15/09//C12Q1/34, (C12N9/78, PC C12N1/21, C12N1/21, C12N15/09//C12Q1/34, C12N9/78, PC C12N1/21, C12N1/21, C12N15/09//C12Q1/34, C12N9/78, PC FT Source

FH Key Location/Qualifiers

FH Key Location/Qualifiers

FT Source / Organism='Alcaligenes faecalis' FT / Organism='Alcaligenes faecalis' FT
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Alcaligenes faecalis gene for creatine amidinohydrolase.
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E16405.1 GI:5711088
JP 1998174585-A/1.
Alcaligenes faecalis
Alcaligenes faecalis
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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Location/Qualifiers
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Best Local Similarity 99.9
Matches 1211; Conservative
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AUTHORS
Sogabe, A., Yamamoto, K. and Kawamura, Y.
TITLE
Gene encoding creatine amidinohydrolase
JOURNAL
TOYOBO CO LTD
PN JP 2001252088-A 1 18-SEP-2001;
PN JP 2001252088-A/1
PD 18-SEP-2001
PF 26-FEB-2001 JP 2001051054
PI ATSUSHI SOGABE, KAZUMI YAMAMOTO, YOSHIHISA KAWAMURA PC C12N15/09, C12N1/21, C12N19/78// (C12N15/09, C12N1/21, PC C12R1:425), C12N15/09, C12R1:425), PC (C1N19/78/C12R1:05), C12N15/00, C12R1:425), CT2N15/00, C12R1:425), PC FT SOURCE
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1. 1277
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AUTHORS
TITLE
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JP 2001252088-A/1.
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                                                                                         ATGACTGACGACATGTTGCACGTGATGAAATGGCACAACGGCGAGAAAGATTATTCGCCG
                                                      TACTGCTATTTCGGACGCAAGTACGGCATGGTCATCGACCACAACAACGCCACGACGATT
                                                                           TTTTCGGATGCCGAGATGACCCGCCGCCAAAACGACGTTCGCGGCTGGATGGCCAAGAAC 120
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Location/Qualifiers
1. .1212
/organism="unidentified"
/mol_type="genomic_DNA"
/db_xref="taxon:32644"
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Best Local Similarity
Matches 1211; Conserv
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Sogabe, A., Nishiya, Y. and Kawamura, Y.

Sogabe, A., Nishiya, Y. and Kawamura, Y.

Scable creatine amidinohydrolase
Patent: JP 2001346594-A 1 18-DEC-2001;

TOYOBO CO LTD

Scable faecalis
PN JP 2001346594-A/1
PD 18-DEC-2001
PP 19-APR-2001 JP 2001121708
PI ATGUSHI SOGABE, YOSHTAKI NISHIYA, YOSHIHISA KAWAMURA PC
C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/80// PC
(C12N9/80,C12R1:05),C12N15/00,C12N5/00
CC Strandedness: Double;
CC Topology: Linear;
CC Stable creatine amidinohydrolase
FH Key Location/Qualifiers
FT source 1.1212

FT source //cyganism='Alcaligenes faecalis'.
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            ACCGACTGGCGCCGCGACAATTTCTATCGCGCCGTGCGCCAGCTGACCACGGGCGCCAAG
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                                                                    TCGGCCGGCATCGACGGCGGCCAGCCCTGGCGCCGCAGCTTCGGCGACAACATCACCTAC
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                                                                                                      CTACCGGGCGTCGACTTCGTCGACATCAGCCAGCCCTCGATGTGGATGCGCACCATCAAG
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Pred. No. 2.6e-145;
0; Mismatches 1;
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                                            Direct Submission
Submitted (05-AUG-1998) Yasuji Koyama, Kikkoman Corporation, Research and Development; Noda 399, Noda, Chiba 278-0037, Ja (B-mail:dai3-kkm@qa2.so-net.ne.jp, Tel:+81-471-23-5571, Fax:+81-471-23-559)
                                                                                          2 (bases 1 to 1215)
Koyama, Y. and Furukawa, K.
Direct Submission
                                                                                                                                     Furukawa,K., Ichikawa,T., Koyama,Y. and Molecular cloning and sequence analysis thermostable creatinase from Alcaligenes
                                                                                                                                                                                              Alcaligenes sp.
Alcaligenes sp.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                           AB016788
Alcaligenes sp.
                                                                                                                                                                                                                                AB016788.1 GI:6681665 creatine amidinohydrolase.
                                                                                                                          Unpublished
                                                                                                                                                                                    Alcaligenaceae; Alcaligenes.
                                                                                                                                                                                                                                                                  strain: KS-85.
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llarity 99.7%;
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/trans1_table=11
/product="creatine amidino
/protein_id="BAA8830.1"
/db_xref="GI:6681666"
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sleeqkliregarvcdvggaacaaaikagvpehevaiattnamireiaksfpfvelmd
tytwfosgintdgahnyvtnrivosgdilslnyffmifgyytaleftlecdhyddasl
diweknvavhrrglelikdgarckdiaielnemyrewdllxyrsfgyghsfguchyy
greagvelredidtelkpgmvvsnepmvmlpegmpgaggyrehdilivgedgaenitg
fpfgfehniirn"
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/db_xref="taxon:512"
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PI FURUKAWA KEISUKE, ICHIKAWA TOSHIO, SUZUKI MASARU, KOYAMA TAIJI PC C12N15/09,C12N9/78 (C12N9/78,C12R1:05),(C12N9/78,C12R1:19); CC strandedness: Double; CC topology: Linear; FH Key Location/Qualifiers
FT source
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E11155.1 GI:220247
JP 1996089255-A/1.
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Furnkawa,K., Ichikawa,T., Suzuki,M. and Koyama,
NOVEL CREATINE AMIDINOHYDROLASE GENE, NOVEL REC
PRODUCTION OF CREATINE AMIDINOHYDROLASE
PREEDLY JP 1996089255-A 1 09-APR-1996;
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Location/Qualifiers
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/db_xref="taxon:32644"
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TCGGCCGGCATCGACGGCGCCAGCCCTGGCGCCGCAGCTTCGGCGACAACATCACCTAC
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TWTWFPQSGINTDGAHMPVTNRIVQSGDILSLNTFPMIFGYTALERTLFCCHYDDASI
DIWEKNVAVHRRGLELIKPGARCKDIAIELNEMYREWDLLKYRSFGYGHSFGVLSHYY
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Patent: EP 1298213-A 17 02-APR-2003;
Roche Diagnostice GmbH (DE) ; F.HOFFMAI
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Variants of an erwinia-type creatinase
Patent: EP 129813.A 9 02-APR-2003;
Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA
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REFERENCE
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                           ATGACTGACGACATGTTGCACGTGATGAAATGGCACAACGGCGAGAAAGATTATTCGCCG
  TTTTCGGATGCCGAGATGACCCGCCGCCAAAACGACGTTCGCGGCTGGATGGCCAAGAAC
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